

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 30, 2002, 12:32:18 : Search time 10 Seconds
(without alignments)
2086.259 Million cell updates/sec

Title: US-10-025-514-16

Perfect score: 2675

Sequence: 1 MEDPQDAQAQKDTSHHDQD.....RDLKCCMGKSCVSPVKA 503

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2030	75.9	418	1	ALAT_HUMAN
2	1894	70.8	409	1	ALAT_PAPAN
3	1491.5	55.8	412	1	ALAT_CALCN
4	1486.5	55.6	421	1	ALAT_PIG
5	1455.5	54.4	411	1	ALAT_RAT
6	1455	54.4	416	1	ALAT_SHEEP
7	1436	53.7	413	1	ALMN_TAMSI
8	1434	53.6	416	1	ALAT_BOVIN
9	1392	52.0	413	1	ALST_TAMSI
10	1388	51.9	413	1	ALSI_TAMSI
11	1376	51.4	413	1	ALMS_TAMSI
12	1338	50.0	413	1	ALAF_RABIT
13	1335	49.9	413	1	ALTI_MOUSE
14	1333	49.8	413	1	ALT2_MOUSE
15	1329	49.7	413	1	ALT3_MOUSE
16	1321	49.4	413	1	HP55_TAMSI
17	1316	49.2	413	1	ALT4_MOUSE
18	1302	48.7	413	1	ALT5_MOUSE
19	1295.5	48.4	412	1	ALAT_MUSCR
20	1293	48.3	405	1	ALAS_CAVPO
21	1266	47.3	403	1	ALAF_CAVPO
22	1246	46.6	410	1	COTR_CAVPO
23	1158.5	43.3	410	1	ALAT_DIDMA
24	1140	42.6	420	1	ALAU_HUMAN
25	849	31.7	423	1	AACT_HUMAN
26	829	31.0	418	1	COTR_MOUSE
27	816	30.5	406	1	CBG_SAISC
28	816	30.5	406	1	IPSP_HUMAN
29	816	30.5	418	1	CP16_RAT
30	816	30.5	427	1	KATN_HUMAN
31	815.5	30.5	405	1	CBG_HUMAN
32	812.5	30.4	416	1	CP11_RAT
33	811	30.3	393	1	CBG_RABIT

34 805 30.1 430 1 CBG_SHEEP
35 804 30.1 417 1 KBP_MOUSE
36 803 30.0 413 1 CFI3_RAT
37 799.5 29.9 412 1 THBG_PIG
38 787.5 29.4 415 1 THBG_HUMAN
39 786.5 29.4 412 1 THBG_SHEEP
40 782.5 29.3 411 1 THBG_BOVIN
41 774.5 29.0 409 1 THBG_RAT
42 771.5 28.8 405 1 IFSP_MOUSE
43 771.5 28.8 418 1 SI24_APOSY
44 739 27.6 372 1 ALAT_CYPCA
45 720.5 26.9 397 1 CBG_MOUSE

P49920 ovls aries
P29621 mus musculus
P05544 rattus norv
Q9tt35 sus scrofa
P05543 homo sapien
P50450 ovls aries
Q9tt36 bos taurus
P35577 rattus norv
P70458 mus musculus
Q60396 apodemus sy
P32759 cyprinus ca
Q06770 mus musculus

ALIGNMENTS

RESULT 1
ALAT_HUMAN
ID ALAT_HUMAN STANDARD; PRT; 418 AA.
AC P01009; QSP1P0; Q13672;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Alpha-1-antitrypsin precursor (Alpha-1 protease inhibitor) (Alpha-1-
DE antiprotease) (PRO0684/PRO2209).
GN SERPINAL OR PI OR AAT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84107980; PubMed=6319097;
RA Bollren A., Herzog A., Cravador A., Herion P., Chuchana P.,
RA van der Straten A., Loriau R., Jacobs P., van Elsen A.;
RT "Cloning and expression in Escherichia coli of full-length
RT complementary DNA coding for human alpha 1-antitrypsin.";
RL DNA 2:255-264 (1983).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=85036645; PubMed=6387509;
RA Rosenberg S., Barr P.J., Najarian R.C., Hallelwell R.A.;
RT "Synthesis in yeast of a functional oxidation-resistant mutant of
RT human alpha-antitrypsin.";
RL Nature 312:77-80(1984).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=85047190; PubMed=6093867;
RA Long G.L., Chandra T., Woo S.L.C., Davie E.W., Kurachi K.;
RT "Complete sequence of the cDNA for human alpha 1-antitrypsin and the
RT gene for the S variant.";
RL Biochemistry 23:4828-4837(1984).
RN [4]
RP SEQUENCE FROM N.A., AND VARIANTS 2.
RX MEDLINE=87057257; PubMed=3491072;
RA Nukiwa T., Satoh K., Brantly M.L., Ogushi F., Fells G.A.,
RA Courtney M., Crystal R.G.;
RT "Identification of a second mutation in the protein-coding sequence
RT of the Z type alpha 1-antitrypsin gene.";
RL J. Biol. Chem. 261:15989-15994(1986).
RN [5]
RP ERRATUM.
RA Nukiwa T., Satoh K., Brantly M.L., Ogushi F., Fells G.A.,
RA Courtney M., Crystal R.G.;
RL J. Biol. Chem. 262:10412-10412(1987).
RN [6]
RP SEQUENCE FROM N.A.
RX MEDLINE=85176977; PubMed=2985281;
RA Ciliberto G., Dente L., Cortese R.;
RT "Cell-specific expression of a transfected human alpha 1-antitrypsin
RT gene.";
RL Cell 41:531-540(1985).

RN [7] SEQUENCE FROM N.A.
RP TISSUE-Fetal liver;
RA Zhang C., Yu Y., Zhang S., Ouyang S., Luo L., Wei H., Zhou G.,
RT Zhou W., Bi J., Zhang Y., Liu M., He F.;
RA "Functional prediction of the coding sequences of 32 new genes deduced
RT by analysis of cDNA clones from human fetal liver."
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
RN [8]
RP SEQUENCE OF 25-418.
RX MEDLINE-82220135; PubMed-7045697;
RA Carrell R.W., Jeppsson J.-O., Laurell C.-B., Brennan S.O., Owen M.C.,
RA Vaughan L., Boswell D.R.;
RT "Structure and variation of human alpha 1-antitrypsin.";
RL Nature 298:329-334(1982).
RN [9]
RP PRELIMINARY SEQUENCE OF 25-418.
RX Chan S.K.;
RA "The covalent structure of human alpha1-protease inhibitor.";
RL Fed. Proc. 41:1016-1016(1982).
RN [10]
RP SEQUENCE OF 1-67; 196-255 AND 387-418 FROM N.A.
RX MEDLINE-82220035; PubMed-6979715;
RA Leicht M., Long G.L., Chandra T., Kurachi K., Kidd V.J., Mace M. Jr.,
RA Davie E.W., Woo S.L.C.;
RT "Sequence homology and structural comparison between the chromosomal
RT human alpha 1-antitrypsin and chicken ovalbumin genes.";
RL Nature 297:655-659(1982).
RN [11]
RP SEQUENCE OF 291-418 FROM N.A.
RX MEDLINE-86005469; PubMed-7031661;
RA Riley J.H., Bathurst I.C., Edbrooke M.R., Carrell R.W., Craig R.K.;
RT "Alpha 1-antitrypsin and serum albumin mRNA accumulation in normal,
RT acute phase and ZZ human liver.";
RL FEBS Lett. 189:361-366(1985).
RN [12]
RP SEQUENCE OF 350-418 FROM N.A.
RX MEDLINE-84292309; PubMed-6332197;
RA Kurachi K., Chandra T., Friezen Degen S.J., White T.T.,
RA Marchioro T.L., Woo S.L.C., Davie E.W.;
RT "Cloning and sequence of cDNA coding for alpha 1-antitrypsin.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:6826-6830(1981).
RN [13]
RP SEQUENCE OF 387-418 FROM N.A.
RX MEDLINE-85225507; PubMed-3873938;
RA Coutelle C., Speer A., Rogers J., Kalsheker N., Humphries S.,
RA Williamson R.;
RT "Construction and partial characterization of a human liver cDNA
RL library.";
RN Biomed. Biochim. Acta 44:421-431(1985).
RN [14]
RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
RX MEDLINE-84292309; PubMed-6332197;
RA Loebermann H., Tokuda R., Deisenhofer J., Huber R.;
RT "Human alpha 1-proteinase inhibitor. Crystal structure analysis of
RT two crystal modifications, molecular model and preliminary analysis
RT of the implications for function.";
RL J. Mol. Biol. 177:531-556(1984).
RN [15]
RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
RX MEDLINE-82221004; PubMed-2785270;
RA Engh R., Loebermann H., Schneider M., Wiegand G., Huber R.,
RA Laurell C.-B.;
RT "The S variant of human alpha 1-antitrypsin, structure and
RT implications for function and metabolism.";
RL Protein Eng. 2:407-415(1989).
RN [16]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE-20386623; PubMed-10933492;
RA Elliott P.R., Pei X.Y., Dafforn T.R., Lomas D.A.;
RT "Topography of a 2.0 A structure of alpha1-antitrypsin reveals targets
RT for rational drug design to prevent conformational disease.";
RL Protein Sci. 9:1274-1281(2000).

RN [17]
RP REVIEW.
RX MEDLINE-89352843; PubMed-2669992;
RA Kalsheker N.;
RT "Alpha 1-antitrypsin: structure, function and molecular biology of
RT the gene.";
RL Biosci. Rep. 9:129-138(1989).
RN [18]
RP REVIEW.
RX MEDLINE-91315455; PubMed-1859394;
RA Wu Y., Foreman R.C.;
RT "The molecular genetics of alpha 1 antitrypsin deficiency.";
RL Bioessays 13:163-169(1991).
RN [19]
RP VARIANT M2.
RX MEDLINE-88324438; PubMed-2901226;
RA Nukiwa T., Brantly M.L., Ogushi F., Fells G.A., Crystal R.G.;
RT "Characterization of the gene and protein of the common alpha 1-
RT antitrypsin normal M2 allele.";
RL Am. J. Hum. Genet. 43:322-330(1988).
RN [20]
RP VARIANT M3.
RX MEDLINE-90368097; PubMed-2394452;
RA Graham A., Hayes K., Weidinger S., Newton C.R., Markham A.F.,
RA Kalsheker N.A.;
RT "Characterisation of the alpha-1-antitrypsin M3 gene, a normal
RT variant.";
RL Hum. Genet. 85:381-382(1990).
RN [21]
RP VARIANT F.
RX MEDLINE-91241132; PubMed-2035534;
RA Okayama H., Brantly M., Holmes M., Crystal R.G.;
RT "Characterization of the molecular basis of the alpha 1-antitrypsin F
RT allele.";
RL Am. J. Hum. Genet. 48:1154-1158(1991).
RN [22]
RP VARIANT M-HEERLEN.
RX MEDLINE-89154435; PubMed-2784123;
RA Hofker M.H., Nukiwa T., van Paassen H.M.B., Nelen M., Kramps J.A.,
RA Klase E.C., Frants R.R., Crystal R.G.;
RT "A Pro-->Leu substitution in codon 369 of the alpha-1-antitrypsin
RT deficiency variant PI M-Heerlen.";
RL Hum. Genet. 81:264-268(1989).
RN [23]
RP VARIANT M-MALTON.
RX MEDLINE-89270478; PubMed-2786335;
RA Fraizer G.C., Harrold T.R., Hofker M.H., Cox D.W.;
RT "In-frame single codon deletion in the M-Malton deficiency allele of
RT alpha 1-antitrypsin.";
RL Am. J. Hum. Genet. 44:894-902(1989).
RN [24]
RP VARIANT M-MINERAL SPRINGS.
RX MEDLINE-90097863; PubMed-1967187;
RA Curiel D.T., Vogelmeier C., Hubbard R.C., Stier L.E., Crystal R.G.;
RT "Molecular basis of alpha 1-antitrypsin deficiency and emphysema
RT associated with the alpha 1-antitrypsin M-Mineral springs allele.";
RL Mol. Cell. Biol. 10:47-56(1990).
RN [25]
RP VARIANT M-NICHINAN.
RX MEDLINE-90178096; PubMed-2309708;
RA Matsunaga E., Shiohara S., Nakamura H., Maruyama T., Tsuda K.,
RA Fukumaki Y.;
RT "Molecular analysis of the gene of the alpha 1-antitrypsin deficiency
RT variant, M-Nichinan.";
RL Am. J. Hum. Genet. 46:602-612(1990).
RN [26]
RP VARIANT M-PROCIDA.
RX MEDLINE-89008457; PubMed-3262617;
RA Takahashi H., Nukiwa T., Satoh K., Ogushi F., Brantly M., Fells G.,
RA Stier L., Courtney M., Crystal R.G.;
RT "Characterization of the gene and protein of the alpha 1-antitrypsin
RT 'deficiency' allele M-Procida.";
RL J. Biol. Chem. 263:15528-15534(1988).

DR	HSP: P01009; 9API.	DR	InterPro; IPR000215; Serpin.
DR	Pfam; PF00079; serpin; 1.	DR	SMART; SM00093; SERPIN; 1.
DR	SMART; SM00284; SERPIN; 1.	DR	Serpin; Serine protease inhibitor; Glycoprotein; Plasma; Signal.
KW	Serpin; Serine protease inhibitor; Glycoprotein; Plasma; Signal.	FT	NON_TER 1
FT	SIGNAL <1 15	FT	CHAIN 16 409
FT	ACT_SITE 373 374	FT	REACTIVE_BOND.
FT	CARBOHYD 61 61	FT	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD 98 98	FT	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD 136 136	FT	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD 262 262	FT	N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ	SEQUENCE 409 AA; 45694 MW; E19B0B7450FDBA9B CRC64;		
Query Match 70.88; Score 1894; DB 1; Length 409;			
Best Local Similarity 92.48; Pred. No. 6.1e-115;			
Matches 364; Conservative 19; Mismatches 11; Indels 0; Gaps			
QY	2 EDPQDAQAQKDTSHHDQHPFNKIPNLAEPFSLYQLAHQSNSTNFIFFSPVSIATA 61		
DB	16 EDPQDAQAQKDTTPHDONHPTLNKITPSLAEFAFSLYQLAHQSNSTNFIFFSPVSIATA 75		
QY	62 FAWLSLGTAKADTHDIELEGNFNFTETPEAQIHGFEQLLRTLNQDLSQLQTGTGNGLFL 121		
DB	76 FAWLSLGTAKADTHSEILEGNFNLTETPEAQVHEGFEQLLRTLNKPSQLQTGTGNGLFL 139		
QY	122 SEGKLVDKFLDYKKLYHSEAFVTFNGDTEEAKKQINDYVEKGQTGKIVOLVKELDRDT 181		
DB	136 NKSLLVVDKFLDYKKNLYHSEAFVTFNGDTEEAKKQINDYVEKGQTGKIVOLVKELDRDT 195		
QY	182 VFALVNYIFFGKVERPEVKDTEEDFHVQDVTTVKVPMMKRLGMEIQHCCKLLSSWVL 241		
DB	196 VFALVNYIFFGKVERPEVATEEEDFHVQDVTTVKVPMMRRLGMEIYHCEKLLSSWVL 255		
QY	242 LMKYLGNAITAFPLPDESKLQHLLENLTHDITTKPLENEDRRSASLHLPKLSITGTYYDLK 301		
DB	256 LMKYLGNAITAFPLPDESKLQHLLENLTHDITTKPLENENRRSANLHLPKLAITGTYYDLK 315		
QY	302 SVLGLGKITKVFSGADLSGVTGEAPLKLKSKAVHKAVLTIDKEGTEAAGANFLAIPMSI 361		
DB	316 TVLGHGLTKVFSGADLSGVTEDAPLKLKSKAVHKAVLTIDKEGTEAAGANFLAIPMSI 375		
QY	362 PPEVFNKPFVFLMEQNTKSPFLFMGKVVNPTOK 395		
DB	376 PPEVFNKPFVFLMEQNTKSPFLFMGKVVNPTOK 409		
RESULT 3			
ALAT_CALCN STANDARD; PRT; 412 AA.			
ID	ALAT_CALCN	AC	054763;
DT	15-JUN-2002 (Rel. 41, Created)	OS	Calloscleriscus caniceps (Gray-bellied squirrel).
DT	15-JUN-2002 (Rel. 41, Last sequence update)	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
DT	15-JUN-2002 (Rel. 41, Last annotation update)	OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Scuridae; Sciurinae;
DE	Alpha-1-antitrypsinase precursor (Alpha-1-antitrypsin) (Alpha-1- trypsinase inhibitor).	OC	Calloscleriscus.
DE	trypsinase inhibitor).	OC	NCBI_TaxID=64664;
OS	Calloscleriscus caniceps (Gray-bellied squirrel).	RN	[1]
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	RP	SEQUENCE FROM N.A.
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Scuridae; Sciurinae;	RC	TISSUE=Liver;
OC	Calloscleriscus.	RC	MEDLINE=98094263; PubMed=9434174;
RN	[1]	RA	Takamatsu N., Kojima M., Taniyama M., Ohba K., Uematsu T., Segawa C.,
RC	TISSUE=Liver;	RA	Tsutsui S., Watanabe M., Kondo J., Kondo N., Shiba T.
RA	Takamatsu N., Kojima M., Taniyama M., Ohba K., Uematsu T., Segawa C.,	RT	"Expression of multiple alpha1-antitrypsin-like genes in hibernating
RT	species of the squirrel family.";	RL	Gene 204:127-132(1997).
RL	Gene 204:127-132(1997).	CC	!- FUNCTION: INHIBITOR OF SERINE PROTEASES (By similarity).

CC -!- SUBCELLULAR LOCATION: Extracellular.
 CC -!- TISSUE SPECIFICITY: PLASMA.
 CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC -----
 CC EMBL; AB000552; BAA24422.1; -
 CC HSP; P01009; 9API.
 CC InterPro: IPR000215; Serpin.
 CC Pfam; PF00079; serpin; 1.
 CC SMART; SM00093; SERPIN; 1.
 CC DR PROSITE; PS00284; SERPIN; 1.
 CC KW Serpin; Serine protease inhibitor; Glycoprotein; Plasma; Signal.
 CC FT SIGNAL 1 24 POTENTIAL.
 CC FT CHAIN 25 412 ALPHA-1-ANTITRYPSINASE.
 CC FT ACT_SITE 377 378 REACTIVE BOND (BY SIMILARITY).
 CC FT CARBOHYD 65 65 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 102 102 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 165 165 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 266 266 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC SQ SEQUENCE 412 AA; 45729 MW; 7235668E9E8FCC6 CRC64;

Query Match 55.88; Score 1491.5; DB 1; Length 412;
 Best Local Similarity 73.58; Pred. No. 5e-89;
 Matches 286; Conservative 45; Mismatches 57; Indels 1; Gaps 1;

QY 6 GDAQAQDTSHDQDHTFNKTPNLAEEAFSLYRLAHQSNSTNIFSPVSIATAFAM 65
 DB 25 GD-AQETDASKDDHEHPACHKIAFNLAEEAFDLYRLARQSNSTNIFSPVSVATAAL 83
 QY 66 SIGTKADTHDELGLNLENLTIPEAQIHGEFQELLTLNQPDQSOLOLTGNGFLSEGL 125
 DB 84 SLGTGKDTHTQILEGLDNLFLNTEPEAQIHGEFQELLTLNQPDQSOLOLTGNGFLDQSL 143
 QY 126 KLVDKFLDVKLVHSEAFVNFQGTAEAKKQINDYVEKGTQKIVDLVRLDRTVFAL 185
 DB 144 KLADKFLDVKLVHSEAFVNFQGTAEAKKQINDYVEKGTQKIVDLVRLDRTVFAL 203
 QY 186 VNYIFFKGKWERPEVKDTEEDFHVQDQVTVKVPMMKRLGMFNQHCCKLSSWVLMKY 245
 DB 204 VNYIFFKGKWERPEVKDTEEDFHVQDQVTVKVPMMKRLGMFNQHCCKLSSWVLMKY 263
 QY 246 LGNATAIFLLPDEGLQHLNLTITKELEDRSASLHLPKLSITGTYDLRSVLS 305
 DB 264 LGNATAIFLLPDEGLQHLNLTITKELEDRSASLHLPKLSITGTYDLRSVLS 323
 QY 306 QIGTKVFSNGADLSGVTEAPLKSVAHVAVLTIDKGTGAAGAFLEAIPMSIPPEV 365
 DB 324 TUGITKVFSEADLSGVTEAPLKSVAHVAVLTIDKGTGAAGAFLEAIPMSIPPEV 383
 QY 366 KFNKPFVFLMIDQNTKSPFLFMGVKNVPTQ 394
 DB 384 REDRPFLLIIIEHYTKSPFLFMGVKNVPTQ 412

RESULT 4
 ALAT_PIG STANDARD; PRG; 421 AA.
 ID ALAT_PIG
 AC P50447;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Alpha-1-antitrypsin precursor (Alpha-1 protease inhibitor) (Alpha-1-
 DE antiprotease).
 GN SERPINA1 OR PI.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

CC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 CC NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=97009792; PubMed=8856896;
 RA Archibald A.L., Couperwhite S., Mellink C.H.M., Lahbib-Mansais Y.,
 RA Gellin J.;
 RT "Porcine alpha-1-antitrypsin (PI): cDNA sequence, polymorphism and
 RT assignment to chromosome 7q2.4-q2.6.";
 RL Anim. Genet. 27:85-89(1996).
 CC -!- FUNCTION: INHIBITOR OF SERINE PROTEASES. ITS PRIMARY TARGET IS
 CC ELASTASE, BUT IT ALSO HAS A MODERATE AFFINITY FOR PLASMIN AND
 CC THROMBIN (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Extracellular.
 CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
 CC -----

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 CC -----

CC EMBL; X88780; CAA61259.1; -
 CC HSP; P01009; 9API.
 CC InterPro: IPR000215; Serpin.
 CC Pfam; PF00079; serpin; 1.
 CC SMART; SM00093; SERPIN; 1.
 CC DR PROSITE; PS00284; SERPIN; 1.
 CC KW Serpin; Serine protease inhibitor; Glycoprotein; Plasma; Signal.
 CC FT SIGNAL 1 24 POTENTIAL.
 CC FT CHAIN 25 421 ALPHA-1-ANTITRYPSIN.
 CC FT ACT_SITE 385 386 REACTIVE BOND.
 CC FT CARBOHYD 73 73 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 110 110 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC SQ SEQUENCE 421 AA; 47194 MW; 08A4AB2A9E600690 CRC64;

Query Match 55.68; Score 1486.5; DB 1; Length 421;
 Best Local Similarity 73.6%; Pred. No. 1.1e-88;
 Matches 292; Conservative 37; Mismatches 65; Indels 3; Gaps 1;

QY 2 EDQPGDAAQKDTSHDQD---HPTFNKITPNLAEEAFSLYRLAHQSNSTNIFSPVSI 58
 DB 25 EGLQGHAVQETDPRHDHGEQEAACHRIAPNLADFAFSLYRQVARQSNSTNIFSPVSI 84
 QY 59 ATAFAMLSLGTAKADTHDELGLNLENLTIPEAQIHGEFQELLTLNQPDQSOLOLTGNG 118
 DB 85 ARAFAMLSLGTAKADTHDELGLNLENLTIPEAQIHGEFQELLTLNQPDQSOLOLTGNG 144
 QY 119 LFLSEGLKLVDFLEDVKLYHSEAFVNFQGTAEAKKQINDYVEKGTQKIVDLVRLD 178
 DB 145 LFTDEKAKLVDFLEDVKLYHSEAFVNFQGTAEAKKQINDYVEKGTQKIVDLVRLD 204
 QY 179 RDVFEALVNYIFFKGKWERPEVKDTEEDFHVQDQVTVKVPMMKRLGMFNQHCCKLSS 238
 DB 205 KDTVFEALVNYIFFKGKWERPEVKDTEEDFHVQDQVTVKVPMMKRLGMFNQHCCKLSS 264
 QY 239 WVLIMKYLGNATAIFLLPDEGLQHLNLTITKELEDRSASLHLPKLSITGTY 298
 DB 265 WVLLMDYVATATAFFLLPDQGLQHLNLTITKELEDRSASLHLPKLSITGTY 324
 QY 299 DLKSVLQGLGITKVFSEADLSGVTEAPLKSVAHVAVLTIDKGTGAAGAFLEAIP 358
 DB 325 DLKSVLQGLGITKVFSEADLSGVTEAPLKSVAHVAVLTIDKGTGAAGAFLEAIP 384
 QY 359 MSTPPEVKFNKPFVFLMIDQNTKSPFLFMGVKNVPTQ 395
 DB 385 MSTPPEVKFNKPFVFLMIDQNTKSPFLFMGVKNVPTQ 421

RESULT 5

AL1AT_RAT
ID AL1AT_RAT STANDARD; PRT; 411 AA.
AC P17475;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE Alpha-1-antitrypsin precursor (Alpha-1-antitrypsin) (Alpha-1-
proteinase inhibitor).
DE Rattus norvegicus (Rat).
OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN
RP SEQUENCE OF 4-411 FROM N.A., AND SEQUENCE OF 25-57.
RC TISSUE=Liver;
RX MEDLINE=90148955; PubMed=2302382;
RA Chao S., Chai K.X., Chao L., Chao J.;
RT "Molecular cloning and sequencing of the cDNA of rat alpha 1-protease
inhibitor and its expression in COS-1 cells.";
RL J. Biochem. 108:230-234(1990).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Liver;
RX MEDLINE=91035351; PubMed=2229024;
RA Misumi Y., Sonda M., Ohkubo K., Takami N., Oda K., Ikehara Y.;
RT "Molecular cloning and sequencing of the cDNA of rat alpha 1-protease
inhibitor and its expression in COS-1 cells.";
RL J. Biochem. 108:230-234(1990).
RN [3]
RP SEQUENCE OF 188-389 FROM N.A.
RC TISSUE=Liver;
RA Flink I.L., Bailey T., Morkin E.;
RL Submitted (AUG-1989) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: INHIBITOR OF SERINE PROTEASES. THE PRIMARY TARGET IS
ELASTASE, BUT ALSO HAS A MODERATE AFFINITY FOR PLASMIN AND
THROMBIN.
CC -1- SUBCELLULAR LOCATION: Extracellular.
CC -1- TISSUE SPECIFICITY: PLASMA.
CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
CC
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CC
CC EMBL; M32247; AAA0788.1; -
DR EMBL; D00675; BAA00579.1; -
DR EMBL; X16273; CAA34349.1; -
DR PIR; A33892; ITRT.
DR HSSP; P01009; 9APT.
DR InterPro; IPR000215; Serpin.
DR Pfam; PF00079; serpin; 1.
DR SMART; SM00093; serpin; 1.
DR PROSITE; PS00284; SERPIN; 1.
KW Serpin; Serine protease inhibitor; Glycoprotein; Plasma; Signal.
FT SIGNAL 1 24
FT CHAIN 25 411 ALPHA-1-ANTITRYPSIN.
FT ACT_SITE 376 377
FT CARBOHYD 64 64 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 101 101 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 265 265 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 14 14 A -> G (IN REF. 2).
FT CONFLICT 84 84 L -> V (IN REF. 2).
FT CONFLICT 247 247 M -> I (IN REF. 3).
FT CONFLICT 248 248 H -> Y (IN REF. 2).
FT CONFLICT 318 318 K -> N (IN REF. 2).
FT CONFLICT 322 322 S -> D (IN REF. 3).
SQ SEQUENCE 411 AA; 46135 MW; B4245CFE21C5C761 CRC64;
Query Match 54.4%; Score 1455.5; DB 1; Length 411;
Best Local Similarity 70.2%; Pred. NO. 1e-86;

Matches 271; Conservative 63; Mismatches 51; Indels 1; Gaps 1;
QY 9 AOKDTSHHQDHPFTFNKITNLAFAFSLYRLAHOSNSTNIEFSPVSIATAFAMLSLG 68
DB 27 AQETDTSQDDQS-PTRYKISSNLADAFPSLYRELHOSNTSNIEFSPMSTITAFAMLSLG 85
QY 69 TKADTHDEILSGNLNTEIPEAOIHGEFOELLARTLNOPDSOLOLTTCNGILFSEGLKLV 128
DB 86 SKGDTKROILLSGLEFNLTQIPEADLHKAFHLLQTLNRPDSELOLNTGNGLVNKNLKV 145
QY 129 DKFLEDDVKLYHSAFTVNFQDTEBAKKQINDYVEKGTQGVKIVDLVKELDRDTVFALVNY 188
DB 146 EKFLVEYKNYHSAFVNFADSEAKKVINDYVEKGTQGVKIVDLVKELDRDTVFALVNY 205
QY 189 IFFGKWERPEFVKDTEEDFHVQVTVTKVPMKRLGMFNHIOCKKLSWVLMKYLGN 248
DB 206 IFFGKWKRPFPNPEHTRDADPHVDKSTTKVPMNRLGMFDMHSTLSSVLMMDYLG 265
QY 249 ATAIFFLPDECKLOHLENELTHDIITKFLNEDRRSASLHLPKLSITGTVDLKSVLQGL 308
DB 266 ATAIFLLPDDGKMOHLEOTLTKDLISRLLRQTRSAIYFPKLSISGTYNLKLTLSSLG 325
QY 309 ITKVFSGADLSGVTETEEAPLKLSKAVHKAVLTIDEKETEAGAMFLAIPMSIPPEVKFN 368
DB 376 ITRVFNDDADLSGITEDAPLKLSQAVHKAVLTLDERTGAAGATVVEAVPMSLPQVKFD 385
QY 369 KPFVFLMIEQNTKSPLEFMGKVVNPQTQ 394
DB 386 HPFIFMIVESETQSPLEFVGKVIDPTR 411

RESULT 6
AL1AT_SHEEP
ID AL1AT_SHEEP STANDARD; PRT; 416 AA.
AC P12725;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE Alpha-1-antitrypsin precursor (Alpha-1-antitrypsin) (Alpha-1-
proteinase inhibitor).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=89366677; PubMed=2788872;
RA Brown W.M., Dziegielewska K.D., Foreman R.C., Saunders N.R., Wu Y.;
RT "Nucleotide and deduced amino acid sequence of sheep alpha 1
antitrypsin.";
RL Nucleic Acids Res. 17:6398-6398(1989).
RN [2]
RP SEQUENCE OF 25-55.
RC TISSUE=Plasma;
RX MEDLINE=9114555; PubMed=1899999;
RA Mistry R., Snashall P.D., Totty N., Guz A., Tetley T.D.;
RT "Isolation and characterization of sheep alpha 1-proteinase
inhibitor.";
RL Biochem. J. 273:685-690(1991).
CC -1- FUNCTION: INHIBITS HUMAN LEUKOCYTE ELASTASE, PIG PANCREATIC
ELASTASE AND BOVINE TRYPSIN ON A 1:1 MOLAR BASIS.
CC -1- SUBCELLULAR LOCATION: Extracellular.
CC -1- TISSUE SPECIFICITY: PLASMA.
CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
CC
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Mon Dec 9 12:50:47 2002

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Db 207 IFFKGKWKQPFNEEQTRKDFHVDKATTVVPMNRLGFMHLHCSTLASVWLQMDYLGN 266
QY 249 ATAIFLDPDEGKLOHLENELTHDITKFLNEDRRSASLHLPKLSITGYDLSKVLGQLG 308
Db 267 ATAIFLDPKGGKQHLEDVTTLLKFLKRNQTSQLYFVKVSIQYDLDKVLSSLG 326
QY 309 ITKFSNGADLSGVTEAPLKLKSKAVHKAVALTIDKGTAAAGAMFLEAPMSPPEVKFN 368
Db 327 ITKVSSEADLSGVTEAPLKLKSKAVHKAVALTIDKGTAAAGAMFLEAPMSPPEVKFN 386
QY 369 KPFVFLMIEONTKSPFMGKVVNPQK 395
Db 387 RPFVLVYIEHHHTKSPFLVGVKNVPTQK 413

RESULT 10
ALMS_TAMSI
ID ALMS_TAMSI STANDARD; PRT; 413 AA.
AC 054760;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Alpha-1-antitrypsin-like protein CM55-SI precursor.
OS Tamas sibiricus (Siberian chipmunk) (Asian chipmunk).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
OC Tamas.
OC NCBI_TaxID=64680;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98094263; PubMed=9434174;
RA Takamatsu N., Kojima M., Taniyama M., Ohba K., Uematsu T., Segawa C.,
RA Tsutou S., Watanabe M., Kondo J., Kondo N., Shiba T.;
RT "Expression of multiple alphas-1-antitrypsin-like genes in hibernating
RT species of the squirrel family."
RL Gene 204:127-132(1997).
CC -!- TISSUE SPECIFICITY: EXPRESSED IN LIVER.
CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY. HIGH, TO ALPHA-1-
CC ANTITRYPSIN.
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CC or send an email to license@isb-sib.ch).
CC EMBL; AB000549; BAA24419.1; -.
CC HSP; P01009; 9API.
CC InterPro: IPR000215; Serpin.
CC Pfam: PF00079; serpin; 1.
CC SMART; SM00093; SERPIN; 1.
CC PROSITE; PS00284; SERPIN; 1.
KW Serpin; Serine protease inhibitor; Glycoprotein; Signal.
FT SIGNAL 1 24
FT CHAIN 25 413
FT MOD_RES 25 25
FT CARBOHYD 102 102
FT CARBOHYD 165 165
FT CARBOHYD 266 266
FT ACT_SITE 377 378
FT REACTIVE_BOND (BY SIMILARITY).
SQ SEQUENCE 413 AA; 46202 MW; AB65A1D31B8CA2EC CRC64;

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Query Match 51.9%; Score 1388; DB 1; Length 413;
 Best Local Similarity 68.2%; Pred. No. 2.3e-82;
 Matches 264; Conservative 59; Mismatches 64; Indels 0; Gaps 0;

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QY 9 AOKDTSHDQDHPTFNKTPNLAFAFSLYRLAQHSNSTNIFSPVSIATAFAMLSLG 68
Db 27 AQETASKDQDEHPASHKTAFLAEFALSFYRLARQSNNTNIFSPVSIATAFAMLSLG 86

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QY 69 TKADTHDEILEGNLNLTEIPEAQIHEGFQELLRLNQPDSQLQTLTNGFLSEGLKLV 128
Db 87 TKGDTHDTLLEGLDNFLNTEMAEADHQGFQHLQLTLNRPNTQLQTLTSGNGLFIDRLNKLK 146
QY 129 DKFLEDVKKLYHSEAFVNFQGTETAEAKQINDYVEKGTQGVKIVDLVKELDRDTFVALVNY 188
Db 147 DKFLEDVKKLYHSEAFVNFQGTETAEAKQINDYVEKGTQGVKIVDLVKELDRDTFVALVNY 206
QY 189 IFFKGKWKQPFNEEQTRKDFHVDKATTVVPMNRLGFMHLHCSTLASVWLQMDYLGN 248
Db 207 IFFKGKWKQPFNEEQTRKDFHVDKATTVVPMNRLGFMHLHCSTLASVWLQMDYLGN 266
QY 249 ATAIFLDPDEGKLOHLENELTHDITKFLNEDRRSASLHLPKLSITGYDLSKVLGQLG 308
Db 267 ATAIFLDPKGGKQHLEDVTTLLKFLKRNQTSQLYFVKVSIQYDLDKVLSSLG 326
QY 309 ITKFSNGADLSGVTEAPLKLKSKAVHKAVALTIDKGTAAAGAMFLEAPMSPPEVKFN 368
Db 327 ITKVSSEADLSGVTEAPLKLKSKAVHKAVALTIDKGTAAAGAMFLEAPMSPPEVKFN 386
QY 369 KPFVFLMIEONTKSPFMGKVVNPQK 395
Db 387 RPFVLVYIEHHHTKSPFLVGVKNVPTQK 413

RESULT 11
ALMS_TAMSI
ID ALMS_TAMSI STANDARD; PRT; 413 AA.
AC 054758;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Alpha-1-antitrypsin-like protein CM55-MS precursor.
OS Tamas sibiricus (Siberian chipmunk) (Asian chipmunk).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
OC Tamas.
OC NCBI_TaxID=64680;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98094263; PubMed=9434174;
RA Takamatsu N., Kojima M., Taniyama M., Ohba K., Uematsu T., Segawa C.,
RA Tsutou S., Watanabe M., Kondo J., Kondo N., Shiba T.;
RT "Expression of multiple alphas-1-antitrypsin-like genes in hibernating
RT species of the squirrel family."
RL Gene 204:127-132(1997).
CC -!- TISSUE SPECIFICITY: EXPRESSED IN LIVER.
CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY. HIGH, TO ALPHA-1-
CC ANTITRYPSIN.
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CC or send an email to license@isb-sib.ch).
CC EMBL; AB000547; BAA24417.1; -.
CC HSP; P01009; 1QLP.
CC InterPro: IPR000215; Serpin.
CC Pfam: PF00079; serpin; 1.
CC SMART; SM00093; SERPIN; 1.
CC PROSITE; PS00284; SERPIN; 1.
KW Serpin; Serine protease inhibitor; Glycoprotein; Signal.
FT SIGNAL 1 24
FT CHAIN 25 413
FT MOD_RES 25 25
FT CARBOHYD 65 65
FT CARBOHYD 102 102
FT CARBOHYD 165 165

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FT CARBOHYD 266 266 N-LINKED (GLCNAC. .) (POTENTIAL).
FT ACT_SITE 377 378 REACTIVE BOND (BY SIMILARITY).
SQ SEQUENCE 413 AA; 45952 MW; 430374CA26EBAF08 CRC64;

Query Match 51.4%; Score 1376; DB 1; Length 413;
Best Local Similarity 68.7%; Pred. No. 1.4e-81;
Matches 266; Conservative 53; Mismatches 68; Indels 0; Gaps 0;

QY 9 AQTDTSHDDHPTNKITPNAEAFSLYROLAHQSNTNFFSPVSIATAFAMLSG 68
DB 27 AQETASQDQDEHPASHRIAPHAEFALSILYRLARQSNTNFFSPVSIATAFAMLSG 86
QY 69 TKADTHDEILEGNFLNLTETPEAQIHGEGFOELLRTLNQPSQLQTLTGNGFLSEGLK 128
DB 87 TKGDTHQILEGLDNLTENAEADIHGFGHLLQTLNRPNTQLTSGNGLFTHQNLKLL 146
QY 129 DKFLEDVKLYHSEAFVNFEGDTEEAQKQINDYVEKGTQKIVDLVKELDRDVFALVNY 188
DB 147 DKFLEDVKLYHSEAFVNFETNMEEAQQINSYVEKGTQKIVELVKELDSDTVALVNY 206
QY 189 IFFKGKWERPEVKDTEEDDFHVDQVTVKVPMMKRLGHFNIOHCKLSWVLLMKYLGN 248
DB 207 IFFKGKWLKFNBEHTREEDFHVDEATTVKVPMMNREGFRHLHHCSTLASWVLMQDYLGN 266
QY 249 ATAIFFLPDGKQLHLENLTHDIITKFLNEDRRSASLHPLKLSITGTVDLKSVLGQLG 308
DB 267 ATAIFLLPDGKQHLQLEDVTSILSKFLNRTTRVSLYFPKVSISGYALKTVLSSLG 326
QY 309 ITRVFSNGADLSGVTEAPLKLKAVHKAVLTIDERGTEAAGAMFLEAIPMSIPPEVKFN 368
DB 327 ITRVFSNAADLSGVTEAPLKLKAVLIDIDEGTEAAGATVGGITFMSRKPKEVIED 386
QY 369 KPFVFLMIEQNTKSPFLPMGKVVNPTQK 395
DB 387 RPFVLIYEHHTKSPFLVGVKVVNPTQK 413

RESULT 12
ALAF_RABIT
ID ALAF_RABIT STANDARD; PRT; 413 AA.
AC P23035;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE Alpha-1-antitrypsinase F precursor (Alpha-1-antitrypsin) (Alpha-1-
DE protease inhibitor) (APF).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91201273; PubMed=2016285;
RA Saito A., Sinohara H.;
RT "Cloning and sequencing of cDNA coding for rabbit alpha-1-
RT antitrypsinase F: amino acid sequence comparison of alpha-1-
RT antitrypsinase of six mammals.";
RL J. Biochem. 109:158-162(1991).
RN [2]
RP SEQUENCE OF 25-41.
RX MEDLINE=88227895; PubMed=3259574;
RA Saito A., Sinohara H.;
RT "Differential interactions of rabbit plasma alpha-1-antitrypsinases S
RT and F with porcine trypsin.";
RL J. Biochem. 103:247-253(1988).
RN [3]
RP SEQUENCE OF 374-380.
RX MEDLINE=91035333; PubMed=2229014;
RA Saito A., Sinohara H.;
RT "Amino acid sequence at the reactive site of rabbit alpha-1-
RT antitrypsinases.";
RL J. Biochem. 108:80-85(1990).
CC -|- FUNCTION: INHIBITOR OF SERINE PROTEASES. THE PRIMARY TARGET IS
```

```
CC ELASTASE, BUT ALSO HAS A MODERATE AFFINITY FOR PLASMIN AND
CC THROMBIN.
CC -|- SUBCELLULAR LOCATION: Extracellular.
CC -|- TISSUE SPECIFICITY: PLASMA.
CC -|- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
CC -----
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CC -----
CC EMBL; X57710; CAA40881.1; -.
CC EMBL; D00853; BAA00728.1; -.
CC PIR; JX0154; JX0154.
CC HSP; P01009; 8AP1.
CC InterPro: IPR000215; Serpin.
CC Pfam: PF00079; serpin; 1.
CC SMART; SM00093; SERPIN; 1.
CC PROSITE; PS00284; SERPIN; 1.
CC Serpin; Serine protease inhibitor; Glycoprotein; Plasma; Signal.
FT SIGNAL 1 24
FT CHAIN 25 413 ALPHA-1-ANTITRYPSINASE F.
FT ACT_SITE 377 378 REACTIVE BOND.
FT CARBOHYD 65 65 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 102 102 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 230 230 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 266 266 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 413 AA; 45867 MW; E851F5DE63A592DF CRC64;

Query Match 50.0%; Score 1338; DB 1; Length 413;
Best Local Similarity 64.9%; Pred. No. 3.8e-79;
Matches 252; Conservative 62; Mismatches 74; Indels 0; Gaps 0;

QY 7 DAAQKTDTSHDDHPTNKITPNAEAFSLYROLAHQSNTNFFSPVSIATAFAMLS 66
DB 25 DEAQETAVSSHEQDHPACHRTAPSLAEFALSILYREVAHESNTNFFSPVSIATAFAMLS 84
QY 67 LGTKADTHDEILEGNFLNLTETPEAQIHGEGFOELLRTLNQPSQLQTLTGNGFLSEGLK 126
DB 85 LGAKGDTHTQVLEGLKFLNLTETAEQIHGDFRHLTLNRPDSEQLAARNALVYHNLK 144
QY 127 LVDFLEDKVLYHSEAFVNFEGDTEEAQKQINDYVEKGTQKIVDLVKELDRDVFALY 186
DB 145 LQHKLEDAKNDYQSEAFVNFDRDPEQAKTINSHVKEGTRGKIVDLVQELDARTLLAY 204
QY 187 NVIFFKGKWERPEVKDTEEDFHVDQVTVKVPMMKRLGHFNIOHCKLSWVLLMKYL 246
DB 205 NVIFFKGKWERPEVKDTEEDFHVDQVTVKVPMMKRLGHFNIOHCKLSWVLLMKYL 264
QY 247 GNATAIFFLPDGEKQLHLENLTHDIITKFLNEDRRSASLHPLKLSITGTVDLKSVLGQ 306
DB 265 GNATAIFFLPDGEKQLHLEDVTSILSKFLNRTTRVSLYFPKVSISGYALKTVLSSLG 324
QY 307 LGITVFSNGADLSGVTEAPLKLKAVHKAVLTIDERGTEAAGAMFLEAIPMSIPPEVK 366
DB 325 LGITVFSNADLSGVTEAPLKLKAVLIDIDEGTEAAGATVGGITFMSRKPKEVIED 384
QY 367 KPFVFLMIEQNTKSPFLPMGKVVNPTQK 394
DB 385 RPFVLIYEHHTKSPFLVGVKVVNPTQK 412

RESULT 13
AL1_MOUSE
ID AL1_MOUSE STANDARD; PRT; 413 AA.
AC P07758;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alpha-1-antitrypsin 1-1 precursor (Serine protease inhibitor 1-1)
```

(Alpha-1 protease inhibitor 1) (Alpha-1-antitrypsin) (AAT).
 Sp11-1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Liver;
 RX MEDLINE=92052104; PubMed=1946354;
 RA Borriello F., Krauter K.S.;
 RT "Multiple murine alpha 1-protease inhibitor genes show unusual
 evolutionary divergence.";
 RL Proc. Natl. Acad. Sci. U.S.A. 88:9417-9421(1991).
 RN [2]
 RP SEQUENCE OF 211-413 FROM N.A.
 RX MEDLINE=86163765; PubMed=3007061;
 RA Krauter K.S., Citron B.A., Hsu M.T., Powell D., Darnell J.E. Jr.;
 RT "Isolation and characterization of the alpha 1-antitrypsin gene of
 mice.";
 RL DNA 5:29-36(1986).
 CC -1- FUNCTION: INHIBITOR OF SERINE PROTEASES. ITS PRIMARY TARGET IS
 ELASTASE, BUT IT ALSO HAS A MODERATE AFFINITY FOR PLASMIN AND
 THROMBIN.
 CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
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 CC -----
 DR EMBL; M75721; AAC28869.1; -;
 DR EMBL; M12586; AAA51624.1; -;
 DR PIR; A25495; A25495.
 DR HSP; P01009; 8AP1.
 DR MGD; MGI:891971; Sp11-1.
 DR InterPro; IPR000215; Serpin.
 DR Pfam; PF000079; serpin; 1.
 DR SMART; SM00093; SERPIN; 1.
 DR PROSITE; PS00284; SERPIN; 1.
 KW Serpin; Serine protease inhibitor; Glycoprotein; Plasma; Signal;
 KW Multigene family.
 FT SIGNAL 1 24 BY SIMILARITY.
 FT CHAIN 25 413 ALPHA-1-ANTITRYPSIN 1-1.
 FT ACT_SITE 377 378 REACTIVE BOND (BY SIMILARITY).
 FT CARBOHYD 64 64 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 101 101 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 265 265 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 246 246 H -> D (IN REF. 2).
 FT CONFLICT 323 323 P -> L (IN REF. 2).
 FT CONFLICT 404 404 L -> V (IN REF. 2).
 SQ SEQUENCE 413 AA; 46002 MW; 1124B2CC356232F4 CRC64;
 Query Match 49.9%; Score 1335; DB 1; Length 413;
 Best Local Similarity 64.3%; Pred. No. 6e-79;
 Matches 249; Conservative 70; Mismatches 66; Indels 2; Gaps 2;
 QY 10 QKTDTHSHDQHTNKNTPNLAEPFSLYQLAHQSNSTIFFSPVSIATAFAMLSLGT 69
 DB 28 QETDTSQKDDQ-PASHEIATNLGDFAISLYRELHVQSNSTIFFSPVSIATAFAMLSLGS 86
 QY 70 KADTHDEILEGLNLFNLTPEAQIHGFGQELLRTLNQDPSQLQTLTGNGFLSGLKLV 129
 DB 87 KGDTHQLEGLQFNLTOTSEADHKSHQHLQTLNRPDSQLQTLTGNGFLVNNDLKLV 146
 QY 130 KFLVDKLYLSEAFVNFVNGTEAKKQINDYVEKGTGKIYDLVKELDRDTVFALVNYI 189
 DB 147 KFLSEAKNHQYAEVSVNFAESEAKKVINDFVEKGTGKTAFAVKLQDQTFVALANYI 206
 QY 190 PFKGWERPFVEKDTDEEDFHVQDVTTKVPMKRLGMFNQHCCKLSSVLLMKYLGN 249

DB 207 LFRGKKKPPDPNTEAEAFHVDSTTKVPMNTLSGMLRHVHCSTLSSVLLMDYAGNA 266
 QY 250 TATFELPDECKLOHLENELTHDIIITKPLENEDRRSASLHLPKLSITGTVDLKSVLGOLGI 309
 DB 267 TAVFLPDDCKMOHLEQTLSEKLSLFLNRRRLAQIHFPRLSISGEYNLKTMSPLGI 326
 QY 310 TKVFSNGADLSGVTEE-APLKLSKAVHKAVLTITDERGTEAAGAMFLEAIPMSIPPEVKFN 368
 DB 327 TRIFNNGADLSGITEENAPLKLSQAVHKAVLTITDEGTEAAAVTVLQWVPMSPILRED 386
 QY 369 KPFFVLMIEQNTKSPFMGKVVNPTOK 395
 DB 387 HPFLFIIEEHTQSPFLGKVVDPETHK 413
 RESULT 14
 ALT2_MOUSE
 ID ALT2_MOUSE STANDARD; PRT; 413 AA.
 AC P22599; Q61283;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Alpha-1-antitrypsin 1-2 precursor (Serine protease inhibitor 1-2)
 DE (Alpha-1 protease inhibitor 2) (Alpha-1-antitrypsin) (AAT).
 GN SP11-2 OR AAT2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90152670; PubMed=2303252;
 RA Sifers R.N., Ledley F.D., Reed-Fourquet L., Ledbetter D.H.;
 RA Ledbetter S.A., Woo S.L.C.;
 RT "Complete cDNA sequence and chromosomal localization of mouse alpha
 1-antitrypsin.";
 RL Genomics 6:100-104(1990).
 RN [2]
 RP SEQUENCE OF 12-413 FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Liver;
 RX MEDLINE=92052104; PubMed=1946354;
 RA Borriello F., Krauter K.S.;
 RT "Multiple murine alpha 1-protease inhibitor genes show unusual
 evolutionary divergence.";
 RL Proc. Natl. Acad. Sci. U.S.A. 88:9417-9421(1991).
 CC -1- FUNCTION: INHIBITOR OF SERINE PROTEASES. ITS PRIMARY TARGET IS
 ELASTASE, BUT IT ALSO HAS A MODERATE AFFINITY FOR PLASMIN AND
 THROMBIN.
 CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
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 CC -----
 DR EMBL; M25529; AAA37132.1; -;
 DR EMBL; M75716; AAC28865.1; -;
 DR HSP; P01009; 8AP1.
 DR MGD; MGI:891970; Sp11-2.
 DR InterPro; IPR000215; Serpin.
 DR Pfam; PF000079; serpin; 1.
 DR SMART; SM00093; SERPIN; 1.
 DR PROSITE; PS00284; SERPIN; 1.
 KW Serpin; Serine protease inhibitor; Glycoprotein; Plasma; Signal;
 KW Multigene family.
 FT SIGNAL 1 24 BY SIMILARITY.
 FT CHAIN 25 413 ALPHA-1-ANTITRYPSIN 1-2.
 FT ACT_SITE 377 378 REACTIVE BOND (BY SIMILARITY).
 FT CARBOHYD 64 64 N-LINKED (GLCNAC. . .) (POTENTIAL).

